SEQUENCE LISTING

<110> Clendennen, Stephanie K.
      Schuster, Debra K.

<120> CTR1 HOMOLOGUE FROM MELON

<130> 4257-0029.30

<140> Not Yet Assigned
<141> Filed Herewith

<150> US 60/218,307
<151> 2000-07-14

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 3286
<212> DNA
<213> Cucumis melo

<220>
<221> misc_feature
<222> (81)...(81)
<223> n = A,T,C or G

<220>
<221> misc_feature
<222> (593)...(594)
<223> n = A,T,C or G

<400> 1
attcgattgt cgggaagaga gagcagaaaa ttaaaaccag aatctccaac acacaaacct   60
tccacccctt caacaatggc nggattctag ggtttctatg ggtttaaggt gatacagttt   120
cctaatttct ccatggaaat gcctggacgg aggtctgatt actctctttt aagtcaaatt   180
ccggacgagg aggttggaac gggagcttcc acttcctttt acgactccgt agcagctggg   240
ggaaacgtta tcaaagggag aaccgatagg gtttttgatt gggatgggag tggtgatcac   300
aggttaaaca cgcaggcgta tcggataggg aacctgtatt catggattgg tttacagaga   360
cattccagtg gaagcagcta cgatgatagc tctctctcta gtgattacta cgcaccgacg   420
ctatcaaacc ctgcagcaaa tgagatcaat gcattggaat atatcctcga tgatgatttc   480
cgagtgatga aagctgtggg aagtggaggt tcgtctggaa agagctgggc ccagcagacg   540
gaagagagct ttcagttgca gcagcccttg gttcttaggc tttcttcaga tgnnacttgt   600
gccgatgatc ccaactttat ggatccgatt ccagacgagg cagctttaag atcgttatcg   660
atttcagctg aggccatctc gcatcggttc tgggtaaatg gatgcatgtc atatttggag   720
aaagtgccag atggtttta tctaattcat gggatggacc catatgtatg gtcattatgc   780
accaatctgc aagaggatgg gcgtatacca tcatttgaat ctctgaaaac agttgattcc   840
agcatcggtt catcaattga agtagttttg atagatcggc atagtgatgc tagcttaaaa   900
gaactgcaaa acagggtgca taatatttct tccagttgtg taaccacaaa agaggttgca   960
gatcatatag caaagctggt atgcaatcac ttggggggtt cagtttctga gggagaagat   1020
gacttggttt ctgcctggaa ggaatgcagc gatgacttaa aggaatgttt gggatctgct   1080
gtgattccct tatgcagctt atctgttggc ctttgtagac atcgtgctct tttattcaaa   1140
gtcctagctg attcaattga tttaccctgt cgaattgcca aaggatgtaa atattgcact   1200
agagatgatg cttcatcttg ccttgttagg ttcgggcttg atagggaata tctcatcgat   1260
ctgattggga ggccaggttg cttatgccaa cctgattctt gctcaatgg tccatcatcc   1320
atctcaattt cttcaccatt gcgatttcca agactaaaac ctattgaatc taccattgat   1380
ttcaggtcac tggccaaaca gtatttcttg gatagccaat cacttaatct tgtatttgat   1440
gaagcttctt caggtaatgt tgtatctggg aaggatgctg cattctccgt ctatcaaagg   1500

1

```
ccattaaata ggaaggatgt agatggaaaa accatagtgg ttactggtga caaggacaga    1560
aattctcagt tattaaataa aaaagcagcc caactgaata ctcaagatgg aaagtctgag    1620
caatttagat catgtgttgc ttctccatat agtgtacagt cgaccccttt tgtagaaaat    1680
gtagtccctt taagccatat ctcacacatt ggttctgaag attcggagca tctcttagca    1740
ttgtctcatc caaggatgga tcatgttaac aatttaccat ttgttcatgg tagtcagttg    1800
attagaaaac caaatgagct ttcccttggc ttagaagatt tggttattcc atggacagat    1860
cttgatttga gggagaaaat tggagcaggt tcttttggga ctgtatatcg tggtgagtgg    1920
catggctctg atgttgctgt gaagatcctc acagaacaag acttccatcc tgaacgtgtt    1980
aatgagtttc tgagagaggt tgctatcatg aaatctttac gacatcctaa tattgtactg    2040
tttatgggtg cggtgaccaa gccaccaaac ttgtccattg tcaccgaata tctatcgaga    2100
ggtagcttgt ataggctttt gcataagtca ggtgtcaaag acatagatga aacacgtcga    2160
ataaatatgg cttttgatgt ggcaaaggga atgaactacc tccacagacg tgatcctcca    2220
attgttcatc gtgatttaaa atcaccgaat ctgttagttg caagaagta tacagtcaag     2280
gtttgtgatt ttggtctctc ccgtttaaag gcacgcacat ttctttcatc caaatctgca    2340
gctggaacac ctgaatggat ggcaccagaa gtactacgcg atgaaccatc aaatgaaaag    2400
tcagatgttt acagctttgg agtgattttg tgggagttgg caactttgca acagccatgg    2460
tgtaatctaa acccagctca ggttgtcgca gctgttggat ttaagggcaa aaggcttgac    2520
atcccacgtg atgtaaatcc caaattggct tccttaatag tggcttgctg ggccgatgag    2580
ccatggaaac gtccttcttt ttccagcatt atggaaacct tgaaaccaat gactaaacaa    2640
gcgccacctc aacaaagtcg cacagacacc ctctcggtta tgtgacaatg tgtgtatcat    2700
aggaatgcct gacgctttgg agggctaagt acggtaccct tcaagagatg tctggcatgt    2760
ttaaaaccat actccaaaca agcaagcacc tgtgctcgta gccaatttt ccattgctag     2820
tagttacaat tttcaagcta agttccttgt accgtgcttc tcaagttttt gtgaacggat    2880
ggggaagtgt tggaaaactt caactgctag acgattccat caaatttatt ctcagttcat    2940
aatcatcaaa atgtagagag attataaaaa tgtggatcac ttcatagtcc acaatcaagg    3000
aagtttctac ctttttgcta tggtgatgaa gaaacttcaa ctccatgtca ccctatttca    3060
cttcacacat tatttgtttg tatatctatt ggtcttacct ttgaggaccg gaccaggaac    3120
taattttgta tatactagtg atcagttgtg gatggatgca atcatgtctt cagtcagact    3180
tggtgtttgc tagggaaata tcattgttgt tatttaacag ccacttcaaa cattcaatta    3240
attttcaccg agtctattat tctaaaaaaa aaaaaaaaa aaaaaa               3286
```

```
<210> 2
<211> 850
<212> PRT
<213> Cucumis melo

<220>
<221> VARIANT
<222> (154)...(154)
<223> Xaa = Any Amino Acid

<400> 2
Met Glu Met Pro Gly Arg Arg Ser Asp Tyr Ser Leu Leu Ser Gln Ile
 1               5                  10                  15
Pro Asp Glu Glu Val Gly Thr Gly Ala Ser Thr Ser Phe Tyr Asp Ser
            20                  25                  30
Val Ala Ala Gly Gly Asn Val Ile Lys Gly Arg Thr Asp Arg Val Phe
        35                  40                  45
Asp Trp Asp Gly Ser Gly Asp His Arg Leu Asn Thr Gln Ala Tyr Arg
    50                  55                  60
Ile Gly Asn Leu Tyr Ser Trp Ile Gly Leu Gln Arg His Ser Ser Gly
65                  70                  75                  80
Ser Ser Tyr Asp Asp Ser Ser Leu Ser Ser Asp Tyr Tyr Ala Pro Thr
                85                  90                  95
Leu Ser Asn Pro Ala Ala Asn Glu Ile Asn Ala Leu Glu Tyr Ile Leu
            100                 105                 110
Asp Asp Asp Phe Arg Val Met Lys Ala Val Gly Ser Gly Gly Ser Ser
            115                 120                 125
Gly Lys Ser Trp Ala Gln Gln Thr Glu Glu Ser Phe Gln Leu Gln Gln
        130                 135                 140
Pro Leu Val Leu Arg Leu Ser Ser Asp Xaa Thr Cys Ala Asp Asp Pro
145                 150                 155                 160
```

                                  2

```
Asn Phe Met Asp Pro Ile Pro Asp Glu Ala Ala Leu Arg Ser Leu Ser
                165             170             175
Ile Ser Ala Glu Ala Ile Ser His Arg Phe Trp Val Asn Gly Cys Met
            180             185             190
Ser Tyr Leu Glu Lys Val Pro Asp Gly Phe Tyr Leu Ile His Gly Met
        195             200             205
Asp Pro Tyr Val Trp Ser Leu Cys Thr Asn Leu Gln Glu Asp Gly Arg
    210             215             220
Ile Pro Ser Phe Glu Ser Leu Lys Thr Val Asp Ser Ser Ile Gly Ser
225             230             235             240
Ser Ile Glu Val Val Leu Ile Asp Arg His Ser Asp Ala Ser Leu Lys
            245             250             255
Glu Leu Gln Asn Arg Val His Asn Ile Ser Ser Ser Cys Val Thr Thr
            260             265             270
Lys Glu Val Ala Asp His Ile Ala Lys Leu Val Cys Asn His Leu Gly
        275             280             285
Gly Ser Val Ser Glu Gly Glu Asp Asp Leu Val Ser Ala Trp Lys Glu
    290             295             300
Cys Ser Asp Asp Leu Lys Glu Cys Leu Gly Ser Ala Val Ile Pro Leu
305             310             315             320
Cys Ser Leu Ser Val Gly Leu Cys Arg His Arg Ala Leu Leu Phe Lys
            325             330             335
Val Leu Ala Asp Ser Ile Asp Leu Pro Cys Arg Ile Ala Lys Gly Cys
            340             345             350
Lys Tyr Cys Thr Arg Asp Asp Ala Ser Ser Cys Leu Val Arg Phe Gly
        355             360             365
Leu Asp Arg Glu Tyr Leu Ile Asp Leu Ile Gly Arg Pro Gly Cys Leu
    370             375             380
Cys Gln Pro Asp Ser Leu Leu Asn Gly Pro Ser Ser Ile Ser Ile Ser
385             390             395             400
Ser Pro Leu Arg Phe Pro Arg Leu Lys Pro Ile Glu Ser Thr Ile Asp
            405             410             415
Phe Arg Ser Leu Ala Lys Gln Tyr Phe Leu Asp Ser Gln Ser Leu Asn
            420             425             430
Leu Val Phe Asp Glu Ala Ser Ser Gly Asn Val Val Ser Gly Lys Asp
            435             440             445
Ala Ala Phe Ser Val Tyr Gln Arg Pro Leu Asn Arg Lys Asp Val Asp
    450             455             460
Gly Lys Thr Ile Val Val Thr Gly Asp Lys Asp Arg Asn Ser Gln Leu
465             470             475             480
Leu Asn Lys Lys Ala Ala Gln Leu Asn Thr Gln Asp Gly Lys Ser Glu
            485             490             495
Gln Phe Arg Ser Cys Val Ala Ser Pro Tyr Ser Val Gln Ser Thr Pro
            500             505             510
Phe Val Glu Asn Val Val Pro Leu Ser His Ile Ser His Ile Gly Ser
            515             520             525
Glu Asp Ser Glu His Leu Leu Ala Leu Ser His Pro Arg Met Asp His
    530             535             540
Val Asn Asn Leu Pro Phe Val His Gly Ser Gln Leu Ile Arg Lys Pro
545             550             555             560
Asn Glu Leu Ser Leu Gly Leu Glu Asp Leu Val Ile Pro Trp Thr Asp
            565             570             575
Leu Asp Leu Arg Glu Lys Ile Gly Ala Gly Ser Phe Gly Thr Val Tyr
            580             585             590
Arg Gly Glu Trp His Gly Ser Asp Val Ala Val Lys Ile Leu Thr Glu
            595             600             605
Gln Asp Phe His Pro Glu Arg Val Asn Glu Phe Leu Arg Glu Val Ala
    610             615             620
Ile Met Lys Ser Leu Arg His Pro Asn Ile Val Leu Phe Met Gly Ala
625             630             635             640
Val Thr Lys Pro Pro Asn Leu Ser Ile Val Thr Glu Tyr Leu Ser Arg
            645             650             655
                                3
```

```
Gly Ser Leu Tyr Arg Leu Leu His Lys Ser Gly Val Lys Asp Ile Asp
            660                 665             670
Glu Thr Arg Arg Ile Asn Met Ala Phe Asp Val Ala Lys Gly Met Asn
            675                 680             685
Tyr Leu His Arg Arg Asp Pro Pro Ile Val His Arg Asp Leu Lys Ser
            690             695         700
Pro Asn Leu Leu Val Asp Lys Lys Tyr Thr Val Lys Val Cys Asp Phe
705             710             715                 720
Gly Leu Ser Arg Leu Lys Ala Arg Thr Phe Leu Ser Ser Lys Ser Ala
                725             730             735
Ala Gly Thr Pro Glu Trp Met Ala Pro Glu Val Leu Arg Asp Glu Pro
            740             745             750
Ser Asn Glu Lys Ser Asp Val Tyr Ser Phe Gly Val Ile Leu Trp Glu
            755             760             765
Leu Ala Thr Leu Gln Gln Pro Trp Cys Asn Leu Asn Pro Ala Gln Val
            770             775             780
Val Ala Ala Val Gly Phe Lys Gly Lys Arg Leu Asp Ile Pro Arg Asp
785             790             795                 800
Val Asn Pro Lys Leu Ala Ser Leu Ile Val Ala Cys Trp Ala Asp Glu
                805             810             815
Pro Trp Lys Arg Pro Ser Phe Ser Ser Ile Met Glu Thr Leu Lys Pro
                820             825             830
Met Thr Lys Gln Ala Pro Pro Gln Gln Ser Arg Thr Asp Thr Leu Ser
            835             840             845
Val Met
    850

<210> 3
<211> 28
<212> DNA
<213> sArtificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 3
caatatttac atccyttggc aattcgac                                        28

<210> 4
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 4
cgtgstgakt ggcatggctc kgatgttgc                                       29

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 5
atgtttggga tctgctgtga ttcc                                            24

<210> 6
<211> 24
```

4

```
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 6
tttggtggct tggtcaccgc accc                                              24

<210> 7
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 7
catgtgttgc ttctccatat agtg                                              24

<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 8
tcatctatgt ctttgacacc tgac                                              24
```

5